

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/525,318  
Source: PG  
Date Processed by STIC: 1/24/06

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 01/24/2006

PATENT APPLICATION: US/10/525,318

TIME: 11:33:03

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\01052006\J525318.raw

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3 <110> APPLICANT: Monsanto Technology LLC
4     Romano, Charles P
5     Bogdanova, Natalia N
7 <120> TITLE OF INVENTION: Nucleotide Sequences Encoding Cry1Bb Proteins for Enhanced
pression in
8     Plants
10 <130> FILE REFERENCE: 38-21(15414)
-> 12 <140> CURRENT APPLICATION NUMBER: US/10/525,318
-> 12 <141> CURRENT FILING DATE: 2005-02-23
12 <150> PRIOR APPLICATION NUMBER: 60/407,428
13 <151> PRIOR FILING DATE: 2002-08-29
15 <160> NUMBER OF SEQ ID NOS: 14
17 <170> SOFTWARE: PatentIn version 3.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 3687
21 <212> TYPE: DNA
22 <213> ORGANISM: Bacillus thuringiensis
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25 <221> NAME/KEY: CDS
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27 <223> OTHER INFORMATION:
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33 <223> OTHER INFORMATION: sequence encoding toxin domain I
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39 <223> OTHER INFORMATION: sequence encoding toxin domain II
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44 <222> LOCATION: (1489)..(1929)
45 <223> OTHER INFORMATION: sequence encoding toxin domain III
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49 <221> NAME/KEY: misc_feature
50 <222> LOCATION: (1930)..(3687)
51 <223> OTHER INFORMATION: sequence encoding protoxin domain
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57 1          5          10          15
59 att cca acg gta tcg aat cct tcc acg caa atg aat cta tca cca gat           96
60 Ile Pro Thr Val Ser Asn Pro Ser Thr Gln Met Asn Leu Ser Pro Asp
61          20          25          30

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65			35					40					45				
67	cca	ttt	ggt	agc	gca	tca	aca	gtc	caa	acg	ggg	ata	aac	ata	gct	ggg	192
68	Pro	Phe	Val	Ser	Ala	Ser	Thr	Val	Gln	Thr	Gly	Ile	Asn	Ile	Ala	Gly	
69			50					55					60				
71	aga	ata	ttg	ggc	gta	tta	ggg	gtg	ccg	ttt	gct	gga	caa	cta	gct	agt	240
72	Arg	Ile	Leu	Gly	Val	Leu	Gly	Val	Pro	Phe	Ala	Gly	Gln	Leu	Ala	Ser	
73	65						70						75			80	
75	ttt	tat	agt	ttt	ctt	ggt	ggg	gaa	tta	tgg	cct	agt	ggc	aga	gat	cca	288
76	Phe	Tyr	Ser	Phe	Leu	Val	Gly	Glu	Leu	Trp	Pro	Ser	Gly	Arg	Asp	Pro	
77						85					90				95		
79	tgg	gaa	att	ttc	ctg	gaa	cat	gta	gaa	caa	ctt	ata	aga	caa	caa	gta	336
80	Trp	Glu	Ile	Phe	Leu	Glu	His	Val	Glu	Gln	Leu	Ile	Arg	Gln	Gln	Val	
81			100						105					110			
83	aca	gaa	aat	act	agg	aat	acg	gct	att	gct	cga	tta	gaa	ggg	cta	gga	384
84	Thr	Glu	Asn	Thr	Arg	Asn	Thr	Ala	Ile	Ala	Arg	Leu	Glu	Gly	Leu	Gly	
85			115					120					125				
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88	Arg	Gly	Tyr	Arg	Ser	Tyr	Gln	Gln	Ala	Leu	Glu	Thr	Trp	Leu	Asp	Asn	
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92	Arg	Asn	Asp	Ala	Arg	Ser	Arg	Ser	Ile	Ile	Leu	Glu	Arg	Tyr	Val	Ala	
93	145					150					155				160		
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96	Leu	Glu	Leu	Asp	Ile	Thr	Thr	Ala	Ile	Pro	Leu	Phe	Arg	Ile	Arg	Asn	
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99	gaa	gaa	ggt	cca	tta	tta	atg	gta	tat	gct	caa	gct	gca	aat	tta	cac	576
100	Glu	Glu	Val	Pro	Leu	Leu	Met	Val	Tyr	Ala	Gln	Ala	Ala	Asn	Leu	His	
101				180						185					190		
103	cta	tta	tta	ttg	aga	gac	gca	tcc	ctt	ttt	ggg	agt	gaa	tgg	ggg	atg	624
104	Leu	Leu	Leu	Leu	Arg	Asp	Ala	Ser	Leu	Phe	Gly	Ser	Glu	Trp	Gly	Met	
105				195				200					205				
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111	gag	gaa	tat	tct	aac	cat	tgc	gta	caa	tgg	tat	aat	aca	ggg	cta	aat	720
112	Glu	Glu	Tyr	Ser	Asn	His	Cys	Val	Gln	Trp	Tyr	Asn	Thr	Gly	Leu	Asn	
113	225					230						235			240		
115	aac	tta	aga	ggg	aca	aat	gct	gaa	agt	tgg	ttg	cgg	tat	aat	caa	ttc	768
116	Asn	Leu	Arg	Gly	Thr	Asn	Ala	Glu	Ser	Trp	Leu	Arg	Tyr	Asn	Gln	Phe	
117						245				250					255		
119	cgt	aga	gac	cta	acg	tta	ggg	gta	tta	gat	tta	gta	gcc	cta	ttc	cca	816
120	Arg	Arg	Asp	Leu	Thr	Leu	Gly	Val	Leu	Asp	Leu	Val	Ala	Leu	Phe	Pro	
121				260				265						270			
123	agc	tat	gat	act	cgc	act	tat	cca	atc	aat	acg	agt	gct	cag	tta	aca	864
124	Ser	Tyr	Asp	Thr	Arg	Thr	Tyr	Pro	Ile	Asn	Thr	Ser	Ala	Gln	Leu	Thr	
125				275				280						285			
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132	Phe	Ala	Ser	Thr	Asn	Trp	Phe	Asn	Asn	Asn	Ala	Pro	Ser	Phe	Ser	Ala	
133	305					310					315					320	
135	ata	gag	gct	gcc	att	ttc	agg	cct	ccg	cat	cta	ctt	gat	ttt	cca	gaa	1008
136	Ile	Glu	Ala	Ala	Ile	Phe	Arg	Pro	Pro	His	Leu	Leu	Asp	Phe	Pro	Glu	
137				325						330					335		
139	caa	ctt	aca	att	tac	agt	gca	tca	agc	cgt	tgg	agt	agc	act	caa	cat	1056
140	Gln	Leu	Thr	Ile	Tyr	Ser	Ala	Ser	Ser	Arg	Trp	Ser	Ser	Thr	Gln	His	
141				340						345					350		
143	atg	aat	tat	tgg	gtg	gga	cat	agg	ctt	aac	ttc	cgc	cca	ata	gga	ggg	1104
144	Met	Asn	Tyr	Trp	Val	Gly	His	Arg	Leu	Asn	Phe	Arg	Pro	Ile	Gly	Gly	
145		355					360					365					
147	aca	tta	aat	acc	tca	aca	caa	gga	ctt	act	aat	aat	act	tca	att	aat	1152
148	Thr	Leu	Asn	Thr	Ser	Thr	Gln	Gly	Leu	Thr	Asn	Asn	Thr	Ser	Ile	Asn	
149		370					375					380					
151	cct	gta	aca	tta	cag	ttt	acg	tct	cga	gac	gtt	tat	aga	aca	gaa	tca	1200
152	Pro	Val	Thr	Leu	Gln	Phe	Thr	Ser	Arg	Asp	Val	Tyr	Arg	Thr	Glu	Ser	
153	385					390					395					400	
155	aat	gca	ggg	aca	aat	ata	cta	ttt	act	act	cct	gtg	aat	gga	gta	cct	1248
156	Asn	Ala	Gly	Thr	Asn	Ile	Leu	Phe	Thr	Thr	Pro	Val	Asn	Gly	Val	Pro	
157				405						410					415		
159	tgg	gct	aga	ttt	aat	ttt	ata	aac	cct	cag	aat	att	tat	gaa	aga	ggc	1296
160	Trp	Ala	Arg	Phe	Asn	Phe	Ile	Asn	Pro	Gln	Asn	Ile	Tyr	Glu	Arg	Gly	
161				420					425					430			
163	gcc	act	acc	tac	agt	caa	ccg	tat	cag	gga	gtt	ggg	att	caa	tta	ttt	1344
164	Ala	Thr	Thr	Tyr	Ser	Gln	Pro	Tyr	Gln	Gly	Val	Gly	Ile	Gln	Leu	Phe	
165			435					440					445				
167	gat	tca	gaa	act	gaa	tta	cca	gaa	aca	aca	gaa	cga	cca	aat	tat		1392
168	Asp	Ser	Glu	Thr	Glu	Leu	Pro	Pro	Glu	Thr	Thr	Glu	Arg	Pro	Asn	Tyr	
169		450					455					460					
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172	Glu	Ser	Tyr	Ser	His	Arg	Leu	Ser	His	Ile	Gly	Leu	Ile	Ile	Gly	Asn	
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175	act	ttg	aga	gca	cca	gtc	tat	tct	tgg	acg	cat	cgt	agt	gca	gat	cgt	1488
176	Thr	Leu	Arg	Ala	Pro	Val	Tyr	Ser	Trp	Thr	His	Arg	Ser	Ala	Asp	Arg	
177				485						490					495		
179	acg	aat	acg	att	gga	cca	aat	aga	att	aca	caa	ata	cca	ttg	gta	aaa	1536
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181				500						505					510		
183	gca	ctg	aat	ctt	cat	tca	ggt	gtt	act	gtt	gtt	gga	ggg	cca	gga	ttt	1584
184	Ala	Leu	Asn	Leu	His	Ser	Gly	Val	Thr	Val	Val	Gly	Gly	Pro	Gly	Phe	
185			515					520					525				
187	aca	ggt	ggg	gat	atc	ctt	cgt	aga	aca	aat	acg	ggt	aca	ttt	gga	gat	1632
188	Thr	Gly	Gly	Asp	Ile	Leu	Arg	Arg	Thr	Asn	Thr	Gly	Thr	Phe	Gly	Asp	
189		530					535						540				
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200	Gly	Thr	Thr	Val	Asn	Ile	Gly	Asn
201				580			585	
203	gat	aat	tta	gaa	tat	aga	agt	ttt
204	Asp	Asn	Leu	Glu	Tyr	Arg	Ser	Phe
205				595			600	
207	ttt	aat	ttt	tta	aat	gcc	caa	agc
208	Phe	Asn	Phe	Leu	Asn	Ala	Gln	Ser
209				610			615	
211	ttt	tca	aat	cag	gaa	gtt	tat	ata
212	Phe	Ser	Asn	Gln	Glu	Val	Tyr	Ile
213	625						630	
215	gag	gta	aca	ttt	gag	gca	gaa	tat
216	Glu	Val	Thr	Phe	Glu	Ala	Glu	Tyr
217				645			650	
219	gtg	aat	gct	ctg	ttt	act	tct	aca
220	Val	Asn	Ala	Leu	Phe	Thr	Ser	Thr
221				660			665	
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224	Val	Thr	Asp	Tyr	His	Ile	Asp	Gln
225				675			680	
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228	Ser	Asp	Glu	Phe	Cys	Leu	Asp	Glu
229				690			695	
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232	Lys	Tyr	Ala	Lys	Arg	Leu	Ser	Asp
233	705						710	
235	aac	ttc	aca	ttc	atc	agt	ggg	caa
236	Asn	Phe	Thr	Phe	Ile	Ser	Gly	Gln
237				725			730	
239	caa	tca	aac	ttc	ccc	tct	att	aat
240	Gln	Ser	Asn	Phe	Pro	Ser	Ile	Asn
241				740			745	
243	gga	agt	gcg	aat	gtt	acc	att	cag
244	Gly	Ser	Ala	Asn	Val	Thr	Ile	Gln
245				755			760	
247	aat	tac	gtc	aca	cta	ccg	ggg	act
248	Asn	Tyr	Val	Thr	Leu	Pro	Gly	Thr
249				770			775	
251	tta	tat	caa	aaa	ata	gga	gag	tca
252	Leu	Tyr	Gln	Lys	Ile	Gly	Glu	Ser
253	785						790	
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257				805			810	

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263	tcc	cta	tgg	ccg	ctt	tca	gtt	gaa	agc	cca	atc	gga	agg	tgc	gga	gaa	2544
264	Ser	Leu	Trp	Pro	Leu	Ser	Val	Glu	Ser	Pro	Ile	Gly	Arg	Cys	Gly	Glu	
265				835				840					845				
267	cca	aat	cga	tgc	gca	cca	cat	ttt	gaa	tgg	aat	cct	gat	cta	gat	tgt	2592
268	Pro	Asn	Arg	Cys	Ala	Pro	His	Phe	Glu	Trp	Asn	Pro	Asp	Leu	Asp	Cys	
269		850					855				860						
271	tcc	tgc	aga	gat	gga	gaa	aga	tgt	gcg	cat	cat	tcc	cat	cat	ttc	act	2640
272	Ser	Cys	Arg	Asp	Gly	Glu	Arg	Cys	Ala	His	His	Ser	His	His	Phe	Thr	
273	865					870				875					880		
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279	tgg	gtg	gta	ttc	aag	att	aag	acg	cag	gaa	ggt	tat	gca	aga	tta	gga	2736
280	Trp	Val	Val	Phe	Lys	Ile	Lys	Thr	Gln	Glu	Gly	Tyr	Ala	Arg	Leu	Gly	
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283	aat	ctg	gaa	ttt	atc	gaa	gag	aaa	cca	tta	att	gga	gaa	gca	ctg	tct	2784
284	Asn	Leu	Glu	Phe	Ile	Glu	Glu	Lys	Pro	Leu	Ile	Gly	Glu	Ala	Leu	Ser	
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288	Arg	Val	Lys	Arg	Ala	Glu	Lys	Lys	Trp	Arg	Asp	Lys	Arg	Glu	Lys	Leu	
289		930				935				940							
291	caa	ttg	gaa	aca	aaa	cga	gta	tat	aca	gag	gca	aaa	gaa	gct	gtg	gat	2880
292	Gln	Leu	Glu	Thr	Lys	Arg	Val	Tyr	Thr	Glu	Ala	Lys	Glu	Ala	Val	Asp	
293	945				950			955					960				
295	gct	tta	ttc	gta	gat	tct	caa	tat	gat	caa	tta	caa	gcg	gat	aca	aac	2928
296	Ala	Leu	Phe	Val	Asp	Ser	Gln	Tyr	Asp	Gln	Leu	Gln	Ala	Asp	Thr	Asn	
297			965				970				975						
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305			995			1000					1005						
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317		1040				1045					1050						
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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/525,318

DATE: 01/24/2006  
TIME: 11:33:04

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\01052006\J525318.raw

valid Line Length:

Rules require that a line not exceed 72 characters in length. This includes spaces.

q#:1; Line(s) 7

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Output Set: N:\CRF4\01052006\J525318.raw

12 M:270 C: Current Application Number differs, Replaced Current Application No  
12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
36 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:27  
1379 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
1385 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
1397 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5  
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